

FILE 'REGISTRY' ENTERED AT 14:37:22 ON 24 OCT 2005

<http://www.cas.org/ONLINE/UG/regprops.html>

=> S RESTRICTION ENZYME/CN
L1 1 RESTRICTION ENZYME/CN

=> D

L1 ANSWER 1 OF 1 REGISTRY COPYRIGHT 2005 ACS on STN
RN 9075-08-5 REGISTRY
ED Entered STN: 16 Nov 1984
CN Nuclease, restriction endodeoxyribo- (9CI) (CA INDEX NAME)
OTHER NAMES:
CN DNA restriction endonuclease
CN DNA restriction enzyme
CN E.C. 3.1.21.4
CN E.C. 3.1.4.32
CN Nuclease, deoxyribonucleic restriction endo-
CN Restriction endodeoxyribonuclease
CN Restriction endonuclease
CN Restriction enzyme
DR 37288-31-6
MF Unspecified
CI MAN
LC STN Files: ADISNEWS, AGRICOLA, BIOBUSINESS, BIOSIS, CA, CAPLUS, CEN,
CHEMLIST, CIN, CSCHEM, IFICDB, IFIPAT, IFIUDB, PROMT, TOXCENTER, USPAT2,
USPATFULL
Other Sources: TSCA**
(**Enter CHEMLIST File for up-to-date regulatory information)

*** STRUCTURE DIAGRAM IS NOT AVAILABLE ***

PROPERTY DATA AVAILABLE IN THE 'PROP' FORMAT

3925 REFERENCES IN FILE CA (1907 TO DATE)
15 REFERENCES TO NON-SPECIFIC DERIVATIVES IN FILE CA
3930 REFERENCES IN FILE CAPLUS (1907 TO DATE)

FILE 'CAPLUS' ENTERED AT 14:37:47 ON 24 OCT 2005

=> S RESTRICTION(W) (ENZYME OR ENDONUCLEASE)
98666 RESTRICTION
12958 RESTRICTIONS
110807 RESTRICTION
(RESTRICTION OR RESTRICTIONS)
752656 ENZYME
435265 ENZYMES
951209 ENZYME
(ENZYME OR ENZYMES)
27056 ENDONUCLEASE
8104 ENDONUCLEASES
31403 ENDONUCLEASE
(ENDONUCLEASE OR ENDONUCLEASES)
L2 32149 RESTRICTION(W) (ENZYME OR ENDONUCLEASE)

=> S L1,L2
3930 L1
L3 32463 (L1 OR L2)

=> S BTGZ1 OR BTGG1 OR (BTGZ(W) (I OR 1))
4 BTGZ1
0 BTGG1

```

0 BTGZ
4126284 I
8437622 1
0 BTGZ(W) (I OR 1)
L4        4 BTGZI OR BTGG1 OR (BTGZ(W) (I OR 1))

=> S BACILLUS;S THERMGLUCOSIDASIUS
86836 BACILLUS
1 BACILLUSES
11922 BACILLI
154 BACILLIS
L5      94950 BACILLUS
(BACILLUS OR BACILLUSES OR BACILLI OR BACILLIS)

0 THERMGLUCOSIDASIUS
L6      0 THERMGLUCOSIDASIUS

=> S GCGATG
L7      2 GCGATG

=> S CGCTAC
L8      0 CGCTAC
0 CGCTAC

=> S L7,L4
L9      5 (L7 OR L4)

```

L9 ANSWER 2 OF 5 CAPLUS COPYRIGHT 2005 ACS on STN
2005:1050685 Document No. 143:320214 Methods for multiplexed single nucleotide polymorphism detection based on restriction-enzyme-mediated single-base extension and capillary electrophoresis. Chen, Xiangning (USA). U.S. Pat. Appl. Publ. US 2005214840 A1 20050929, 24 pp.

(English). CODEN: USXXCO. APPLICATION: US 2005-86401 20050323.
PRIORITY: US 2004-2004/PV555357 20040323.

AB A method for single nucleotide polymorphism (SNP) genotyping using widely available DNA sequencers is provided. This method uses a type II restriction enzyme to create extendable ends at target polymorphic sites and uses single-base extension (SBE) to discriminate alleles. In this design, a restriction site is engineered in one of the two polymerase chain reaction (PCR) primers so that the restriction endonuclease cuts immediately upstream of the targeted SNP site. The digestion of the PCR products generates a 5'-overhang structure at the targeted polymorphic site. This 5'-overhang structure then serves as a template for SBE reaction to generate allele-specific products using fluorescent dye-terminator nucleotides. Following the SBE, the allele-specific products with different sizes can be resolved by DNA sequencers. Through primer design, a series of PCR products that vary in size and contain only one restriction enzyme recognition site are created. This allows many PCR products to be loaded in a single capillary/lane. Restriction-enzyme-mediated single-base extension is demonstrated by typing multiple SNPs simultaneously for 44 DNA samples. By multiplexing PCR and pooling multiplexed reactions together, this method has the potential to score 50-100 SNPs/capillary/run if the sizes of PCR products are arranged at every 5-10 bases from 100 to 600 base range.

L9 ANSWER 3 OF 5 CAPLUS COPYRIGHT 2005 ACS on STN

2005:260235 Document No. 142:330781 Method for gene identification signature (GIS) analysis for gene discovery and genome mapping. Ruan, Yijun; Ng, Patrick; Wei, Chialin (Agency for Science, Technology and Research, Singapore). PCT Int. Appl. WO 2005026391 A1 20050324, 88 pp. DESIGNATED STATES: W: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BW, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NA, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW; RW: AT, BE, BF, BJ, CF, CG, CH, CI, CM, CY, DE, DK, ES, FI, FR, GA, GB, GR, IE, IT, LU, MC, ML, MR, NE, NL, PT, SE, SN, TD, TG, TR. (English). CODEN: PIXXD2. APPLICATION: WO 2004-SG298 20040916. PRIORITY: US 2003-2003/664234 20030917.

AB An isolated oligonucleotide comprising at least one ditag, wherein the ditag comprises two joined first and second sequence tags, wherein the first tag comprises the 5'-terminus sequence and the second tag comprises the 3'-terminus sequence of a nucleic acid mol. or a fragment thereof. GIS anal. is developed using a DNA tag sequencing with the concept of paired-end ditagging and mapping strategy, in which 5' and 3' signatures of full-length cDNAs are accurately extracted into paired-end ditags (PETs) that are concatenated for efficient sequencing and mapped to genome sequences to demarcate the transcription boundaries of every gene. GIS anal. is potentially 30-fold more efficient than standard cDNA sequencing approaches for transcriptome characterization. The invention demonstrates this approach with 116,252 PET sequences derived from mouse embryonic stem cells. Initial anal. of this dataset identifies hundreds of previously uncharacterized transcripts, including alternative transcripts of known genes. The invention also uncovers several intergenically spliced and unusual fusion transcripts, one of which is confirmed as a trans-splicing event and is differentially expressed. The ditag anal. is useful for gene discovery and genome mapping.

L9 ANSWER 4 OF 5 CAPLUS COPYRIGHT 2005 ACS on STN

2004:421876 Document No. 141:65840 A multiplexing single nucleotide polymorphism typing method based on restriction-enzyme-mediated single-base extension and capillary electrophoresis. Che, Yihua; Chen, Xiangning (Virginia Institute for Psychiatric and Behavioral Genetics and Department of Psychiatry, Virginia Commonwealth University, Richmond, VA, 23298, USA). Analytical Biochemistry, 329(2), 220-229 (English) 2004. CODEN: ANBCA2. ISSN: 0003-2697. Publisher: Elsevier Science.

AB Millions of single nucleotide polymorphisms (SNPs) have been identified in recent years. This provides a great opportunity for large-scale association and population studies. However, many high-throughput SNP typing techniques require expensive and dedicated instruments, which render them out of reach for many labs. To meet the need of these labs., we here report a method that uses widely available DNA sequencer for SNP typing. This method uses a type II restriction enzyme to create extendable ends at target polymorphic sites and uses single-base extension (SBE) to discriminate alleles. In this design, a restriction site is engineered in one of the two polymerase chain reaction (PCR) primers so that the restriction endonuclease cuts immediately upstream of the targeted SNP site. The digestion of the PCR products generates a 5'-overhang structure at the targeted polymorphic site. This 5'-overhang structure then serves as a template for SBE reaction to generate allele-specific products using fluorescent dye-terminator nucleotides. Following the SBE, the allele-specific products with different sizes can be resolved by DNA sequencers. Through primer design, we can create a series of PCR products that vary in size and contain only one restriction enzyme recognition site. This allows us to load many PCR products in a single capillary/lane. This method, restriction-enzyme-mediated single-base extension, is demonstrated by typing multiple SNPs simultaneously for 44 DNA samples. By multiplexing PCR and pooling multiplexed reactions together, this method has the potential to score 50-100 SNPs/capillary/run if the sizes of PCR products are arranged at every 5-10 bases from 100 to 600 base range.

L9 ANSWER 5 OF 5 CAPLUS COPYRIGHT 2005 ACS on STN
2000:555738 Document No. 134:55022 Predominance of a 6 bp deletion in exon 2 of the LDL receptor gene in Africans with familial hypercholesterolemia. Thiart, Rochelle; Scholtz, Charlotte L.; Vergotine, Joseph; Hoogendijk, Christiaan F.; De Villiers, J. Nico P.; Nissen, Henrik; Brusgaard, Klaus; Gaffney, Dairena; Hoff, Michael S.; Vermaak, W. J. Hayward; Kotze, Maritha J. (MRC Cape Heart Group, Division of Human Genetics, Faculty of Medicine, University of Stellenbosch, Tygerberg, S. Afr.). Journal of Medical Genetics, 37(7), 514-519 (English) 2000. CODEN: JMDGAE. ISSN: 0022-2593. Publisher: BMJ Publishing Group.

AB In South Africa, the high prevalence of familial hypercholesterolemia (FH) among Afrikaners, Jews, and Indians as a result of founder genes is in striking contrast to its reported virtual absence in the black population in general. In this study, the mol. basis of primary hypercholesterolemia was studied in 16 Africans diagnosed with FH. DNA anal. using three screening methods resulted in the identification of seven different mutations in the coding region of the low d. lipoprotein (LDLR) gene in 10 of the patients analyzed. These included a 6 bp deletion (GCCATG) accounting for 28% of defective alleles, and six point mutations (D151H, R232W, R385Q, E387K, P678L, and R793Q) detected in single families. The Sotho patient with missense mutation R232W was also heterozygous for a de novo splicing defect 313+1G→A. Several silent mutations/polymorphisms were detected in the LDLR and apolipoprotein B genes, including a base change (g→t) at nucleotide position -175 in the FP2 LDLR regulatory element. This promoter variant was detected at a significantly higher ($p<0.05$) frequency in FH patients compared to controls and occurred in cis with mutation E387K in one family. Anal. of four intragenic LDLR gene polymorphisms showed that the same chromosomal background was identified at this locus in the four FH patients with the 6 bp deletion. Detection of the 6 bp deletion in Xhosa, Pedi, and Tswana FH patients suggests that it is an ancient mutation predating tribal separation approx. 3000 yr ago.

=> S THERMOGLUCOSIDASIUS
L10 71 THERMOGLUCOSIDASIUS

=> S L10 AND L3
L11 2 L10 AND L3

=> S L11 NOT L9
L12 1 L11 NOT L9

=> D CBIB ABS

L12 ANSWER 1 OF 1 CAPLUS COPYRIGHT 2005 ACS on STN
1998:48003 Document No. 128:178068 Strain differentiation and taxonomic characterization of a thermophilic group of phenol-degrading bacilli. Duffner, Fiona M.; Reinscheid, Uwe M.; Bauer, Michael P.; Mutzel, Astrid; Mueller, Rudolf (Technical Univ. Hamburg-Harburg, Hamburg, D-21073, Germany). Systematic and Applied Microbiology, 20(4), 602-611 (English) 1997. CODEN: SAMIDF. ISSN: 0723-2020. Publisher: Gustav Fischer Verlag.
AB Thirteen new thermophilic phenol degrading strains were isolated from a number of geog. distinct thermal sources. The strains demonstrated similar growth characteristics with pH optima between 6.0-7.2, temperature optima between 60°-70° and similar substrate utilization spectra. The comparison of chromosomal restriction endonuclease, ribotyping, and total cellular protein patterns in addition to bacteriocin typing was used for strain differentiation and resulted in the formation of 5 different groups to which the isolates were assigned. Eight of the isolates were assigned to group 2 based on identical patterns generated for each method applied. Addnl. methods such as the comparison of antibiotic MIC values, phenol tolerance, co-metabolic transformation of chlorophenols, fatty acid Me ester (FAME) patterns, and RFLP patterns revealed minor differences between the isolates of group 2. Isolate A2, of this group and A7, which displayed differences using every technique applied, were selected for taxonomic identification and were identified as *B. thermoleovorans* and *B. thermoglucosidasius*, resp. This is the 1st report of phenol degrading isolates belonging to these species.

=> E MORGAN R/AU

=> S E3,E7,E8,E75,E79,E80

77 "MORGAN R"/AU
8 "MORGAN R D"/AU
1 "MORGAN R DONALD"/AU
45 "MORGAN RICHARD"/AU
44 "MORGAN RICHARD D"/AU
1 "MORGAN RICHARD DAVID"/AU

L13 176 ("MORGAN R"/AU OR "MORGAN R D"/AU OR "MORGAN R DONALD"/AU OR "MORGAN RICHARD"/AU OR "MORGAN RICHARD D"/AU OR "MORGAN RICHARD DAVID"/AU)

=>

=> E WALSH P/AU

=> S E3,E45-E52

31 "WALSH P"/AU
3 "WALSH PAUL"/AU
1 "WALSH PAUL F"/AU
3 "WALSH PAUL J"/AU
1 "WALSH PAUL JUDE"/AU
1 "WALSH PAUL P"/AU
12 "WALSH PAUL R"/AU
1 "WALSH PAUL RAYMOND"/AU
1 "WALSH PAUL S"/AU

L14 54 ("WALSH P"/AU OR "WALSH PAUL"/AU OR "WALSH PAUL F"/AU OR "WALSH PAUL J"/AU OR "WALSH PAUL JUDE"/AU OR "WALSH PAUL P"/AU OR "WALSH PAUL R"/AU OR "WALSH PAUL RAYMOND"/AU OR "WALSH PAUL S"/AU)

=> S L13,L14

L15 229 (L13 OR L14)

=> S L15 AND L3

L16 52 L15 AND L3

=> S L16 AND L5
L17 7 L16 AND L5

=> S L17 NOT (L9,L12)
L18 6 L17 NOT ((L9 OR L12))

=> D 1-6 CBIB ABS

L18 ANSWER 1 OF 6 CAPLUS COPYRIGHT 2005 ACS on STN
2001:51325 Document No. 134:233508 Characterization of the specific DNA nicking activity of restriction endonuclease N.BstNBI.
Morgan, Richard D.; Calvet, Celine; Demeter, Matthew; Agra, Rafael; Kong, Huimin (New England Biolabs, Beverly, MA, 01915, USA). Biological Chemistry, 381(11), 1123-1125 (English) 2000. CODEN: BICHF3. ISSN: 1431-6730. Publisher: Walter de Gruyter GmbH & Co. KG.

AB N.BstNBI is a unique restriction endonuclease isolated from *Bacillus stearothermophilus*. We have characterized the recognition sequence and the cleavage site of N.BstNBI. Mapping of cleavage sites of N.BstNBI showed that it recognizes an asym. sequence, 5' GAGTC 3', and cleaves only on the top strand 4 base pairs away from its recognition sequence. To verify the nicking activity of N.BstNBI, we have constructed two plasmids containing a single recognition sequence (pNB1) or no recognition site (pNBO). When pNB1 and pNBO were incubated with the enzyme, N.BstNBI nicked only the plasmid pNB1, suggesting that N.BstNBI is a specific nicking endonuclease.

L18 ANSWER 2 OF 6 CAPLUS COPYRIGHT 2005 ACS on STN
1996:622077 Document No. 125:295786 BaeI, another unusual BcgI-like restriction endonuclease. Sears, Lauren E.; Zhou, Bing; Aliotta, Jason M.; Morgan, Richard D.; Kong, Huimin (New England Biolabs, Inc., Beverly, MA, 01915, USA). Nucleic Acids Research, 24(18), 3590-3592 (English) 1996. CODEN: NARHAD. ISSN: 0305-1048. Publisher: Oxford University Press.

AB BcgI and BcgI-like restriction endonucleases have a very distinct characteristic which causes them to differ from the other classified restriction enzymes; they all cleave double-stranded DNA specifically on both sides of the recognition sequence to excise a short DNA fragment including the recognition sites. Here we report a new BcgI-like restriction endonuclease, BaeI, isolated from *Bacillus sphaericus*. Like BcgI, BaeI also cleaves double-stranded DNA on both strands upstream and downstream of its recognition sequence (10/15)ACNNNNGTAYC(12/7). There are two dominant polypeptides in the final preparation of BaeI with mol. masses of .apprx.80 and 55 kDa. Both are slightly larger than the two BcgI subunits. BaeI requires both Mg²⁺ and AdoMet to cleave DNA. Accompanying bilateral cleavage activity, the heteromeric BaeI also has an N6-adenine methyltransferase activity which modifies the sym. located adenines within its recognition sequence.

L18 ANSWER 3 OF 6 CAPLUS COPYRIGHT 2005 ACS on STN
1993:228789 Document No. 118:228789 A unique restriction endonuclease, BcgI, from *Bacillus coagulans*. Kong, Huimin; Morgan, Richard D.; Maunus, Robert E.; Schildkraut, Ira (New England Biolabs, Inc., Beverly, MA, 01915, USA). Nucleic Acids Research, 21(4), 987-91 (English) 1993. CODEN: NARHAD. ISSN: 0305-1048.

AB A new restriction endonuclease, BcgI, which has properties unlike those of the three recognized classes of restriction enzymes, was purified and characterized. BcgI was isolated from *Bacillus coagulans*, and it recognizes the sequence CGAN6TGC. BcgI cleaves double stranded DNA on both strands upstream and downstream of the recognition sequence, so that the recognition sequence is released as a 34-base pair fragment with 2-base 3'-extensions. Mg²⁺ and S-adenosylmethionine are required for cleavage. Sinefungin, a structural analog of AdoMet which generally inhibits methylase activity, can replace AdoMet in the

cleavage reaction. The apparent binding constant (K_{Apb}) for AdoMet is about 100 nM, while the K_{appb} for sinefungin is about 500 nM.

- L18 ANSWER 4 OF 6 CAPLUS COPYRIGHT 2005 ACS on STN
1990:473476 Document No. 113:73476 Identification of a new type II restriction endonuclease, BsaAI. Kong, Huimin; Morgan, Richard D.; Chen, Zhongfu (New England Biolabs, Inc., Beverly, MA, 01915, USA). Nucleic Acids Research, 18(9), 2832 (English) 1990. CODEN: NARHAD. ISSN: 0305-1048.
AB A new type II restriction endonuclease, BsaAI, was isolated from *Bacillus stearothermophilus* G668. BsaAI recognizes and cleaves the palindromic sequence 5'-pyrimidine-AC/GT-purine-3'. BsaAI cleaves in the middle of its recognition sequence to produce blunt-ended fragments. The optimum reaction conditions for BsaAI are: 100 mM NaCl, 50 mM tris-HCl (pH 7.5), 10 mM MgCl₂, 37°.

- L18 ANSWER 5 OF 6 CAPLUS COPYRIGHT 2005 ACS on STN
1990:174516 Document No. 112:174516 A new type II restriction endonuclease, BsmAI, from *Bacillus stearothermophilus*. Kong, Huimin; Morgan, Richard D.; Chen, Zhongfu (New England Biolabs, Inc., Beverly, MA, 01915, USA). Nucleic Acids Research, 18(3), 686 (English) 1990. CODEN: NARHAD. ISSN: 0305-1048.
AB BsmAI is a unique restriction endonuclease from *B. stearothermophilus* NEB 529 which recognizes 5'-GTCTC-3'. It cleaves 1 nucleotide 3' of the recognition sequence on one strand and 5 nucleotides 3' of the recognition sequence on the opposite strand to generate a 4-base 5'-extension. BsmAI cleaved pBR322 at 3 sites, which were mapped to positions 2150, 3450, and 4200 with BamHI and PstI. These positions all contained the sequence, 5'-GTCTC-3'. The predicted fragment sizes generated by cleavage of phage λ, phage T7 and adenovirus 2 DNAs at the sequence, 5'-GTCTC-3' matched the observed fragment sizes from BsmAI digests of these DNAs, from which it was concluded that BsmAI recognizes the sequence, 5'-GTCTC-3'.

- L18 ANSWER 6 OF 6 CAPLUS COPYRIGHT 2005 ACS on STN
1988:469273 Document No. 109:69273 Bsrl, a unique restriction endonuclease from *Bacillus stearothermophilus* which recognized 5'ACTGG3'. Polisson, Carol; Morgan, Richard D. (New England Biolabs, Beverly, MA, 01915, USA). Nucleic Acids Research, 16(11), 5205 (English) 1988. CODEN: NARHAD. ISSN: 0305-1048.
AB A new type II restriction endonuclease, Bsrl, was isolated from *B. stearothermophilus*. Bsrl recognizes the 5 base nonpalindromic sequence 5'-ACTGG-3'. It cleaves 1 nucleotide outside of the recognition sequence on 1 strand, and within the recognition sequence on the opposite strand, to generate a 2 base 3' overhang.

	L #	Hits	Search Text	DBs
1	L1	56864	RESTRICTION ADJ (ENZYME OR ENDONUCLEASE)	US- PGPUB; USPAT
2	L2	39609	BACILLUS	US- PGPUB; USPAT
3	L3	35	THERMOGLUCOSIDASIUS	US- PGPUB; USPAT
4	L4	6	BTGZI OR BTGZ1 OR (BTGZ ADJ (1 OR I))	US- PGPUB; USPAT
5	L5	12	L3 AND L1	US- PGPUB; USPAT
6	L6	11	GCGATG	US- PGPUB; USPAT
7	L7	10	CGCTAC	US- PGPUB; USPAT
8	L8	18	(L6 OR L7) AND L1	US- PGPUB; USPAT
9	L9	3	(L6 OR L7) NOT L8	US- PGPUB; USPAT

Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	0	(restriction adj (endonuclease or enzyme))".clm"	US-PGPUB; USPAT	ADJ	ON	2005/10/24 15:51
L2	2954	(restriction adj (endonuclease or enzyme)).CLM.	US-PGPUB; USPAT	ADJ	ON	2005/10/24 15:51
L3	5	BACILLUS THERMOGLUCOSIDASIUS CLM.	US-PGPUB; USPAT	ADJ	ON	2005/10/24 15:51

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OM protein - protein search, using sw model

Run on: October 19, 2005, 18:31:52 ; Search time 166 Seconds
(without alignments)
62.907 Million cell
updates/sec

Title: US-10-617-361-8
Perfect score: 132
Sequence: 1 MYWLLDYVTQQKVRNDINNLIKXILXI 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : A_Geneseq_16Dec04:*

- 1: geneseqp1980s:*
- 2: geneseqp1990s:*
- 3: geneseqp2000s:*
- 4: geneseqp2001s:*
- 5: geneseqp2002s:*
- 6: geneseqp2003as:*
- 7: geneseqp2003bs:*
- 8: geneseqp2004s:*

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 19, 2005, 18:35:13 ; Search time 16 Seconds
(without alignments)
162.366 Million cell
updates/sec

Title: US-10-617-361-8
Perfect score: 132
Sequence: 1 MYWLLDYVTQQKVRNDINNLIKXILXI 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : PIR_79:
1: pir1:
2: pir2:
3: pir3:
4: pir4:

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 19, 2005, 18:34:53 ; Search time 57 Seconds
(without alignments)
242.564 Million cell
updates/sec.

Title: US-10-617-361-8
Perfect score: 132
Sequence: 1 MYWLLDYVTQQKVRNDINNLIKXILXI 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : UniProt_03:
1: uniprot_sprot:
2: uniprot_trembl:

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 19, 2005, 18:35:59 ; Search time 22 Seconds
(without alignments)
91.615 Million cell
updates/sec

Title: US-10-617-361-8
Perfect score: 132
Sequence: 1 MYWLLDYVTQQKVRNDINNLIKXILXI 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Issued_Patents_AA:
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:

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OM protein - protein search, using sw model

Run on: October 19, 2005, 18:41:05 ; Search time 167 Seconds
(without alignments)
67.392 Million cell
updates/sec

Title: US-10-617-361-8
Perfect score: 132
Sequence: 1 MYWLLDYVTQQKVRNDINNLIKXILXI 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1860064 seqs, 416830855 residues

Total number of hits satisfying chosen parameters: 1860064

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Published_Applications_AA:*

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep:*

7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*

8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*

9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep:*

10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep:*

11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep:*

12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*

13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*

14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep:*

16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep:*

17: /cgn2_6/ptodata/1/pubpaa/US10E_PUBCOMB.pep:*

18: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*

19: /cgn2_6/ptodata/1/pubpaa/US11A_PUBCOMB.pep:*

20: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*

21: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

22: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

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OM protein - protein search, using sw model

Run on: October 19, 2005, 18:37:09 ; Search time 498 Seconds
(without alignments)
63.326 Million cell
updates/sec

Title: US-10-617-361-8
Perfect score: 132
Sequence: 1 MYWLLDYVTQQKVRNDINNLIKXILXI 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 6959266 seqs, 1168006243 residues

Total number of hits satisfying chosen parameters: 6959266

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database :

Pending_Patents_AA_Main:*

- 1: /cgn2_6/ptodata/1/paa/PCTUS_COMB.pep:*
- 2: /cgn2_6/ptodata/1/paa/US06_COMB.pep:*
- 3: /cgn2_6/ptodata/1/paa/US07_COMB.pep:*
- 4: /cgn2_6/ptodata/1/paa/US080_COMB.pep:*
- 5: /cgn2_6/ptodata/1/paa/US081_COMB.pep:*
- 6: /cgn2_6/ptodata/1/paa/US082_COMB.pep:*
- 7: /cgn2_6/ptodata/1/paa/US083_COMB.pep:*
- 8: /cgn2_6/ptodata/1/paa/US084_COMB.pep:*
- 9: /cgn2_6/ptodata/1/paa/US085_COMB.pep:*
- 10: /cgn2_6/ptodata/1/paa/US086_COMB.pep:*
- 11: /cgn2_6/ptodata/1/paa/US087_COMB.pep:*
- 12: /cgn2_6/ptodata/1/paa/US088_COMB.pep:*
- 13: /cgn2_6/ptodata/1/paa/US089_COMB.pep:*
- 14: /cgn2_6/ptodata/1/paa/US090_COMB.pep:*
- 15: /cgn2_6/ptodata/1/paa/US091_COMB.pep:*
- 16: /cgn2_6/ptodata/1/paa/US092_COMB.pep:*
- 17: /cgn2_6/ptodata/1/paa/US093_COMB.pep:*
- 18: /cgn2_6/ptodata/1/paa/US094_COMB.pep:*
- 19: /cgn2_6/ptodata/1/paa/US095_COMB.pep:*
- 20: /cgn2_6/ptodata/1/paa/US096_COMB.pep:*
- 21: /cgn2_6/ptodata/1/paa/US097A_COMB.pep:*
- 22: /cgn2_6/ptodata/1/paa/US097B_COMB.pep:*
- 23: /cgn2_6/ptodata/1/paa/US098_COMB.pep:*
- 24: /cgn2_6/ptodata/1/paa/US099A_COMB.pep:*
- 25: /cgn2_6/ptodata/1/paa/US099B_COMB.pep:*
- 26: /cgn2_6/ptodata/1/paa/US100_COMB.pep:*
- 27: /cgn2_6/ptodata/1/paa/US101_COMB.pep:*
- 28: /cgn2_6/ptodata/1/paa/US102_COMB.pep:*
- 29: /cgn2_6/ptodata/1/paa/US103_COMB.pep:*
- 30: /cgn2_6/ptodata/1/paa/US104_COMB.pep:*
- 31: /cgn2_6/ptodata/1/paa/US105_COMB.pep:*
- 32: /cgn2_6/ptodata/1/paa/US106_COMB.pep:*
- 33: /cgn2_6/ptodata/1/paa/US107_COMB.pep:*
- 34: /cgn2_6/ptodata/1/paa/US108_COMB.pep:*
- 35: /cgn2_6/ptodata/1/paa/US109_COMB.pep:*
- 36: /cgn2_6/ptodata/1/paa/US110_COMB.pep:*
- 37: /cgn2_6/ptodata/1/paa/US60_COMB.pep:*

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OM protein - protein search, using sw model

Run on: October 19, 2005, 18:40:09 ; Search time 86 Seconds
(without alignments)
63.343 Million cell
updates/sec

Title: US-10-617-361-8
Perfect score: 132

Sequence: 1 MYWLLDYVTQQKVRNDINNLIKXILXI 27

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 897115 seqs, 201758920 residues

Total number of hits satisfying chosen parameters: 897115

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 500 summaries

Database : Pending_Patents_AA_New:*

1: /cgn2_6/ptodata/1/paa/PCT_NEW_COMB.pep:*

2: /cgn2_6/ptodata/1/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/1/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/1/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/1/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/1/paa/US10_NEW_COMB.pep:*

7: /cgn2_6/ptodata/1/paa/US11_NEW_COMB.pep:*

8: /cgn2_6/ptodata/1/paa/US60_NEW_COMB.pep:*